



# UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
-----------------	-------------	----------------------	---------------------	------------------

10/786,501

02/25/2004

Susan L. Acton

MPI98-052P1RDV10DV1M

3988

30405

7590

07/05/2007

MILLENNIUM PHARMACEUTICALS, INC.

40 Landsdowne Street

CAMBRIDGE, MA 02139

EXAMINER

SANG, HONG

ART UNIT

PAPER NUMBER

1643

MAIL DATE

DELIVERY MODE

07/05/2007

PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Interview Summary</b>	<b>Application No.</b>	<b>Applicant(s)</b>	
	10/786,501	ACTON, SUSAN L.	
	<b>Examiner</b>	<b>Art Unit</b>	
	Hong Sang	1643	

All participants (applicant, applicant's representative, PTO personnel):

(1) Hong Sang. (3)\_\_\_\_\_.

(2) Mario Cloutier. (4)\_\_\_\_\_.

Date of Interview: 25 June 2007.

Type: a) ☒ Telephonic b) ☐ Video Conference  
c) ☐ Personal [copy given to: 1) ☐ applicant 2) ☐ applicant's representative]

Exhibit shown or demonstration conducted: d) ☐ Yes e) ☐ No.

If Yes, brief description: \_\_\_\_\_.

Claim(s) discussed: \_\_\_\_\_.

Identification of prior art discussed: \_\_\_\_\_.

Agreement with respect to the claims f) ☐ was reached. g) ☐ was not reached. h) ☒ N/A.

Substance of Interview including description of the general nature of what was agreed to if an agreement was reached, or any other comments: see continuation sheet.

(A fuller description, if necessary, and a copy of the amendments which the examiner agreed would render the claims allowable, if available, must be attached. Also, where no copy of the amendments that would render the claims allowable is available, a summary thereof must be attached.)

THE FORMAL WRITTEN REPLY TO THE LAST OFFICE ACTION MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW. (See MPEP Section 713.04). If a reply to the last Office action has already been filed, APPLICANT IS GIVEN A NON-EXTENDABLE PERIOD OF THE LONGER OF ONE MONTH OR THIRTY DAYS FROM THIS INTERVIEW DATE, OR THE MAILING DATE OF THIS INTERVIEW SUMMARY FORM, WHICHEVER IS LATER, TO FILE A STATEMENT OF THE SUBSTANCE OF THE INTERVIEW. See Summary of Record of Interview requirements on reverse side or on attached sheet.

Examiner Note: You must sign this form unless it is an Attachment to a signed Office action.

\_\_\_\_\_  
Examiner's signature, if required

## Summary of Record of Interview Requirements

### Manual of Patent Examining Procedure (MPEP), Section 713.04, Substance of Interview Must be Made of Record

A complete written statement as to the substance of any face-to-face, video conference, or telephone interview with regard to an application must be made of record in the application whether or not an agreement with the examiner was reached at the interview.

#### Title 37 Code of Federal Regulations (CFR) § 1.133 Interviews Paragraph (b)

In every instance where reconsideration is requested in view of an interview with an examiner, a complete written statement of the reasons presented at the interview as warranting favorable action must be filed by the applicant. An interview does not remove the necessity for reply to Office action as specified in §§ 1.111, 1.135. (35 U.S.C. 132)

#### 37 CFR §1.2 Business to be transacted in writing.

All business with the Patent or Trademark Office should be transacted in writing. The personal attendance of applicants or their attorneys or agents at the Patent and Trademark Office is unnecessary. The action of the Patent and Trademark Office will be based exclusively on the written record in the Office. No attention will be paid to any alleged oral promise, stipulation, or understanding in relation to which there is disagreement or doubt.

The action of the Patent and Trademark Office cannot be based exclusively on the written record in the Office if that record is itself incomplete through the failure to record the substance of interviews.

It is the responsibility of the applicant or the attorney or agent to make the substance of an interview of record in the application file, unless the examiner indicates he or she will do so. It is the examiner's responsibility to see that such a record is made and to correct material inaccuracies which bear directly on the question of patentability.

Examiners must complete an Interview Summary Form for each interview held where a matter of substance has been discussed during the interview by checking the appropriate boxes and filling in the blanks. Discussions regarding only procedural matters, directed solely to restriction requirements for which interview recordation is otherwise provided for in Section 812.01 of the Manual of Patent Examining Procedure, or pointing out typographical errors or unreadable script in Office actions or the like, are excluded from the interview recordation procedures below. Where the substance of an interview is completely recorded in an Examiner's Amendment, no separate Interview Summary Record is required.

The Interview Summary Form shall be given an appropriate Paper No., placed in the right hand portion of the file, and listed on the "Contents" section of the file wrapper. In a personal interview, a duplicate of the Form is given to the applicant (or attorney or agent) at the conclusion of the interview. In the case of a telephone or video-conference interview, the copy is mailed to the applicant's correspondence address either with or prior to the next official communication. If additional correspondence from the examiner is not likely before an allowance or if other circumstances dictate, the Form should be mailed promptly after the interview rather than with the next official communication.

The Form provides for recordation of the following information:

- Application Number (Series Code and Serial Number)
- Name of applicant
- Name of examiner
- Date of interview
- Type of interview (telephonic, video-conference, or personal)
- Name of participant(s) (applicant, attorney or agent, examiner, other PTO personnel, etc.)
- An indication whether or not an exhibit was shown or a demonstration conducted
- An identification of the specific prior art discussed
- An indication whether an agreement was reached and if so, a description of the general nature of the agreement (may be by attachment of a copy of amendments or claims agreed as being allowable). Note: Agreement as to allowability is tentative and does not restrict further action by the examiner to the contrary.
- The signature of the examiner who conducted the interview (if Form is not an attachment to a signed Office action)

It is desirable that the examiner orally remind the applicant of his or her obligation to record the substance of the interview of each case. It should be noted, however, that the Interview Summary Form will not normally be considered a complete and proper recordation of the interview unless it includes, or is supplemented by the applicant or the examiner to include, all of the applicable items required below concerning the substance of the interview.

A complete and proper recordation of the substance of any interview should include at least the following applicable items:

- 1) A brief description of the nature of any exhibit shown or any demonstration conducted,
- 2) an identification of the claims discussed,
- 3) an identification of the specific prior art discussed,
- 4) an identification of the principal proposed amendments of a substantive nature discussed, unless these are already described on the Interview Summary Form completed by the Examiner,
- 5) a brief identification of the general thrust of the principal arguments presented to the examiner,  
(The identification of arguments need not be lengthy or elaborate. A verbatim or highly detailed description of the arguments is not required. The identification of the arguments is sufficient if the general nature or thrust of the principal arguments made to the examiner can be understood in the context of the application file. Of course, the applicant may desire to emphasize and fully describe those arguments which he or she feels were or might be persuasive to the examiner.)
- 6) a general indication of any other pertinent matters discussed, and
- 7) if appropriate, the general results or outcome of the interview unless already described in the Interview Summary Form completed by the examiner.

Examiners are expected to carefully review the applicant's record of the substance of an interview. If the record is not complete and accurate, the examiner will give the applicant an extendable one month time period to correct the record.

#### Examiner to Check for Accuracy

If the claims are allowable for other reasons of record, the examiner should send a letter setting forth the examiner's version of the statement attributed to him or her. If the record is complete and accurate, the examiner should place the indication, "Interview Record OK" on the paper recording the substance of the interview along with the date and the examiner's initials.

Examiner called applicants' representative Mario Cloutier regarding submitting a paper copy of sequence listing and a statement that the paper copy and the CRF are identical and that no new matter has been introduced. Applicants faxed the following documents to the examiner.

1. paper copy of sequence listing.
2. a statement that the paper copy and the CRF are identical and that no new matter has been introduced.

See attached fax documents.

Hong Sang, Ph.D.  
Art Unit 1643  
June 25, 2007

Burden Hour Statement: This form is estimated to take 0.03 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time required to complete this form should be sent to , Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

In re application of:	Susan L. Acton		
Application No.:	10/786,501	Group No.:	1643
Filed:	February 25, 2004	Examiner:	SANG, HONG
For:	CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3) ANTIBODIES (as amended)		

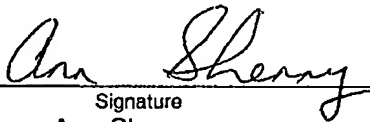
Practitioner's Docket No. MPI98-052P1RDV10DV1M

PATENT

## Certificate of Transmission under 37 CFR 1.8

1-571-273 8145

I hereby certify that this correspondence is being facsimiled transmitted to the  
United States Patent and Trademark Office

on June 25, 2007.

Signature

Ann Sherry

Typed or printed name of person signing Certificate

Note: Each paper must have its own certificate of transmission, or this certificate must identify  
each submitted paper.

**Submitted herewith:**

This Certificate of Transmission under 37 CFR 1.8

1 page

Submission of Sequence Listing

4 pages

Paper Copy of Sequence Listing

31 pages

Total (including Fax Transmittal)

36 pages

TO/SB/97 (08-00)

Approved for use through 10/31/2002. OMB 0651-0031

U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it contains a valid OMB control number.

Practitioner's Docket No. MPI98-052P1RDV10DV1M

PATENT

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Susan L. Acton		
Application No.:	10/786,501	Group No.:	1643
Filed:	February 25, 2004	Examiner:	SANG, HONG
For:	CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3) ANTIBODIES (as amended)		

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY,  
AND/OR AMENDMENT PERTAINING THERETO  
FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE  
AND/OR AMINO ACID SEQUENCE

1. This submission accompanies the new application being filed concurrently herewith

## IDENTIFICATION OF PERSON MAKING STATEMENT

2. I, Mario Cloutier

(type or print name of person signing below)

state the following:

## CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10\*

I hereby certify that, on the date shown below, this correspondence is being:

## MAILING

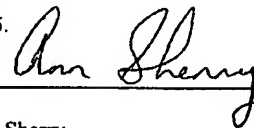
- ☐ deposited with the United States Postal Service in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.  
37 C.F.R. SECTION 1.8(a) 37 C.F.R. SECTION 1.10\*

- ☐ with sufficient postage as first class mail. ☐ as "Express Mail Post Office to Addressee"  
Mailing Label No.

## TRANSMISSION

- ☒ transmitted by facsimile to the Patent and Trademark Office at 1-571-273 8145.

Signature



Ann Sherry

(type or print name of person certifying)

\*WARNING: Each paper or fee filed by "Express Mail" must have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. section 1.10(b). "Since the filing of correspondence under section 1.10 without the Express Mail mailing label thereon is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will not be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.

(Page 1 of 4)

Practitioner's Docket No. MPI98-052P1RDV10DV1M

ITEMS BEING SUBMITTED

3. Submitted herewith are:

- A. ☐ "Sequence Listing(s)" for the nucleotide and/or amino acid sequence(s) in this application. Each sequence in the "Sequence Listing" is assigned a separate identifier as required in 37 C.F.R. Section 1.821(c) and 37 C.F.R. Sections 1.822 and 1.823.
- B. ☐ An amendment to the description and/or claims, wherein reference is made to the sequence by use of the assigned identifier, as required in 37 C.F.R. Section 1.821(d).
- C. ☐ A copy of each "Sequence Listing" submitted for this application in computer readable form, in accordance with the requirements of 37 C.F.R. Sections 1.821(e) and 1.824.
- D. ☒ Paper copy of "Sequence Listing" corresponding to the electronic copy of "Sequence Listing" on file in present application.

In re application of:			
Application No.:			
Filed:			
For:			

The Computer readable form(s) of applicant's other application corresponds to the "Sequence Identifier(s)" of the application as follows:

Computer Readable Form

"Sequence Identifier"

(other application)

(this application)

- E. ☒ A statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same, as required in 37 C.F.R. Section 1.821(g).
- ☐ Because the statement is not made by a person registered to practice before the Office, the Statement is verified as required in 37 C.F.R. Section 1.821(b).
- F. ☐ Because this submission is made in fulfilling the requirement under 37 C.F.R. Section 1.821(g), a statement that the submission includes no new matter.
- ☐ Because the statement is not made by a person registered to practice before the Office, the statement is verified, as required in 37 C.F.R. Section 1.821(g).

Practitioner's Docket No. MPI98-052P1RDV10DV1M

**STATEMENTS REGARDING THE SEQUENCE LISTING SUBMITTED HERewith**

4. I hereby state:

- A. ☒ Each computer readable form submitted in this application, including those forms requested to be transferred from applicant's other application, is the same as the "Sequence Listing" to which it is indicated to relate.
- B. ☒ All papers accompanying this submission, or for which a request for transfer from applicants' other application, introduce no new matter.

**EXTENSION OF TERM**

5. The proceedings herein are for a patent application and the provisions of 37 C.F.R. Section 1.136 apply.

- (a) ☐ Applicant petitions for an extension of time under 37 C.F.R. Section 1.136 (fees: 37 C.F.R. Section 1.17(a)(1)-(4)) for the total number of months checked below:

Extension (months)	Fee for other than small entity	Fee for small entity
<input type="checkbox"/> one month	\$ 120.00	\$ 60.00
<input type="checkbox"/> two months	\$ 450.00	\$ 225.00
<input type="checkbox"/> three months	\$1,020.00	\$ 510.00
<input type="checkbox"/> four months	\$1,590.00	\$ 795.00

Fee \$0.00

If an additional extension of time is required, please consider this a petition therefor.

- ☐ An extension for \_\_\_\_\_ months has already been secured, and the fee paid therefor of \$0.00 is deducted from the total fee due for the total months of extension now requested.

Extension fee due with this request \$0.00

**OR**

- (b) ☒ Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition and fee for extension of time.

(Page 3 of 4)



Practitioner's Docket No. MPI98-052P1RDV10DV1M

**FEE PAYMENT**

6. ☐ Attached is a check in the sum of \$ \_\_\_\_\_.
- ☐ Charge Account No. \_\_\_\_\_ the sum of \$0.00  
A duplicate of this transmittal is attached.

**FEE DEFICIENCY**

7. ☐ If any additional extension and/or fee is required, charge Account No. \_\_\_\_\_.

8. Correspondence Address

Direct all future correspondence to:

Customer Number 30405

OR

Intellectual Property Department  
MILLENNIUM PHARMACEUTICALS, INC.  
40 Landsdowne Street  
Cambridge, MA 02139

June 25, 2007

MILLENNIUM PHARMACEUTICALS, INC.

By Mario Cloutier

Mario Cloutier

Registration No. 57,225

40 Landsdowne Street

Cambridge, MA 02139

Telephone - 617-577-3522

Facsimile - 617-551-8820

80

## SEQUENCE LISTING

&lt;110&gt; Acton, Susan

&lt;120&gt; NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

&lt;130&gt; MNI-050

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 15

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 4137

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; 'n' at positions 2872, 3597 and 3682 may be any nucleic acid

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (297)..(1202)

&lt;400&gt; 1

```

tcgacccacg cgtccgggag gatcgggagt cgcgggagga tgggccgccg ctaggctcgc 60
actccggacg cgcctcgcag tgcgcagggt gggtgccccg cgcctgcagc gtccgccggg 120
gcgggcgccg gggagggtggc cgacaggctc cgggcctcgc agcctcagcc cccggccccag 180
cgcgctttcc gacggcgggc cgcgcgccag ccaccgccc gcccaaggtc tctcgggggc 240
gggagaacgg aaaactccca acttcctgag ttctaaagtt cctgttgctt cagaca atg 299
                                         Met
                                         1
gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347
Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
      5              10              15
cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395
Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
      20              25              30
ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443
Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
      35              40              45
aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491
Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
      50              55              60              65
cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539

```

81

Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys	
70 75 80	
gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat	587
Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr	
85 90 95	
tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta	635
Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu	
100 105 110	
gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag caa	683
Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln	
115 120 125	
aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt	731
Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu	
130 135 140 145	
tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat	779
Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg Asp	
150 155 160	
ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt	827
Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu	
165 170 175	
gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca	875
Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala	
180 185 190	
cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat	923
His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His	
195 200 205	
gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta	971
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu	
210 215 220 225	
cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg	1019
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met	
230 235 240	
aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca cct	1067
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro	
245 250 255	
ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat atg	1115
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met	
260 265 270	
tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt tat	1163
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr	
275 280 285	
gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca	1212
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser	

82

290	295	300	
agatcatgaa	gagtgttaacc	aaagtaattg	aaagtatttt gtgcaaagtc gtacctscce 1272
atttatgtct	gggtgttaag	attaatat	cagagctagt gtgctctgaa tccttaacca 1332
gttttcatat	aagcttcatt	ttgtaccagt	cacctaaatc acctccttgc aacccccaaa 1392
tgactttgga	ataactgaat	tgcatgttag	gagagaaaat gaaacatgat ggttttgaat 1452
ggctaaaggt	ttatagaatt	tcttacagtt	ttctgctgat aaattgtgtt tagatagact 1512
gtcagtgcca	aatattgaag	gtgcagcttg	gcacacatca gaatagactc atacctgaga 1572
aaaagtatct	gaacatgtga	cttgtttctt	tttttagtaat ttatggacat tgagatgaac 1632
acaattgtga	acttttgtga	agattttatt	tttaaacggt tgaagtacta gtttttagttc 1692
ttagcagagt	agttttcaaa	tatgattctt	atgataaatg tagacacaaa ctatttgaga 1752
aacatttaga	actcttagct	tatacattca	aatgttaact attaaatgtg aagatttggg 1812
gacaaaatgt	gagtcagaca	ctgaagagtt	ttttgttttg ttttaatat tttgatattc 1872
tctttgcatt	gaaatgggtat	aatgaatcc	atttaaaaag tggttaagga tttgttttagc 1932
tgggtgtgata	ataattttta	aagttgcaca	ttgcccaagg ctttttttgt gtgtttttat 1992
tgttgtttgt	acatttgaaa	aatattcttt	gaataacctt gcagtactat atttcaagrt 2052
ttctttataa	atttaagtgc	attttaactc	ataattgtac actataatat aagcctaagt 2112
ttttattcat	aagttttatt	gaagttctga	tcggtccctc tcagaaattt ttttatatta 2172
ttcttcaagt	tactttctta	tttatattgt	atgtgcattt tatccattaa tgtttcatac 2232
tttctgagag	tataataccc	ttttaaaga	tatttggtat accaatactt ttcctggatt 2292
gaaaactttt	tttaactttt	ttaaaatttg	ggccactctg tatgcatatg tttggtcttg 2352
ttaaagagga	agaaaggatg	tgtgtttatac	tgtacctgtg aatgttgata cagttacaat 2412
ttatttgaca	aggttgtaat	tctagaatat	gcttaataaa atgaaaactg gccatgacta 2472
cagccagaac	tgttatgaga	ttaacatttc	tattgagaag cttttgagta aagtactgta 2532
tttgttcatg	aagatgactg	agatggtaac	acttcgtgta gcttaaggaa atgggcagaa 2592
tttcgtaaat	gctgttgtgc	agatgtgttt	tccctgaatg ctttcgtatt agtggcgacc 2652
agtttctcac	agaattgtga	agcctgaagy	ccaagaggaa gtcactgtta aaggaactctg 2712
tgccatctta	caaccttgga	tgaattatcc	tgccaacgtg aaaacctcat gttcaaagaa 2772
cacttccctt	tagccgatgt	aactgctggt	tttgtttttc atatgtgttt ttcttacact 2832
catttgaatg	ctttcaagca	tttgtaaact	taaaaaaaaan wawaaagggc aaaaagtctg 2892

83

aacccttggtt ttctgaaatc taatcagtta tgtatgggtt ctgaagggtta attttatttt 2952  
ggaataggta aagcgaaacc tggtttgtcw tgtttttccct gagggctaga tgcatttttt 3012  
ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072  
agtatgagaa gaattattct tattgaccat taatgtcatg ttcattttta tgtaatatata 3132  
ttgagatgaa atgttctctg gttggaacag atactctctt ttttttctt gcaatcttta 3192  
agaatacata gatctaaaat tcattagctt gaccctcaa agtaactttt aagtaaagat 3252  
taaagctttt cttctcagtg aatatatctg ctagaaggaa atagctggga agaatttaat 3312  
gatcaggga attcattatt tctatatgtg gaaacttttt gcttcgaata ttgtatcttt 3372  
ttaaactctaa atgttcatat ttttctgaa gaaaccactg tgtaaaaatc aaatttttaat 3432  
tttgaatgga ataatttcaa agaactatga agatgatttg aagctctaatt ttatatagtc 3492  
acctataaaa tgttctttat atgtgttcat aagtaaattt tatattgatt aagttaaact 3552  
tttgaattga ttgaggagc agtaaaatga aagctatatc tattnctaaa ccytatttag 3612  
acattggkac cagttacca gytgaaaata kggagtaact ttgttttgta tggtaagggt 3672  
taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732  
tgtaaattha gtaagatatt acagccattt catgaatgct ttaccattca acatagtatc 3792  
tattacaaaa cacctttctt gtatccatat acttcagggtg ttgctgttaa catttactat 3852  
gatattttatt ttaacacaaa tgttactcac attaaatggt tattctttta aatgaatgta 3912  
ttatgttttt aaccacacaaa tgcataactta cctgtgcct catatttcaa tagtactgta 3972  
atatggacat cttttgtgaa atacttttat tttgttatgc tttaaatata catacaaaaa 4032  
gatttctgtt attagctttg aaaattgtat aatatcctaa tataacaaaa atataaaaaat 4092  
aaaaatgaat acagtaaaaa aaaaaaaaaa aaaaaaaaaa aaagg 4137

&lt;210&gt; 2

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe  
1 5 10 15

Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala  
20 25 30

Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val

84

35                      40                      45  
 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys  
     50                      55                      60  
 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile  
     65                      70                      75                      80  
 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys  
                     85                      90                      95  
 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu  
                     100                      105                      110  
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys  
                     115                      120                      125  
 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln  
                     130                      135                      140  
 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg  
     145                      150                      155                      160  
 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys  
                     165                      170                      175  
 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala  
                     180                      185                      190  
 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile  
                     195                      200                      205  
 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys  
                     210                      215                      220  
 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys  
     225                      230                      235                      240  
 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro  
                     245                      250                      255  
 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn  
                     260                      265                      270  
 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val  
                     275                      280                      285  
 Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser  
                     290                      295                      300

&lt;210&gt; 3

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

85

&lt;221&gt; CDS

&lt;222&gt; (1)..(906)

&lt;400&gt; 3

atg gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc	48
Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe	
1 5 10 15	
caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc	96
Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala	
20 25 30	
aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt	144
Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val	
35 40 45	
tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa	192
Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys	
50 55 60	
gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc	240
Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile	
65 70 75 80	
aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa	288
Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys	
85 90 95	
tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa	336
Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu	
100 105 110	
cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag	384
Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys	
115 120 125	
caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag	432
Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln	
130 135 140	
ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga	480
Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg	
145 150 155 160	
gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa	528
Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys	
165 170 175	
ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct	576
Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala	
180 185 190	
gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata	624
Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile	
195 200 205	
cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt	672

86

His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys  
 210 215 220  
 cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa 720  
 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys  
 225 230 235 240  
 atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca 768  
 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro  
 245 250 255  
 cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat 816  
 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn  
 260 265 270  
 atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt 864  
 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val  
 275 280 285  
 tat gac gta gca aag agg atg cat gca tgc act gca agc agc 906  
 Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser  
 290 295 300  
  
 <210> 4  
 <211> 2120  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (47)..(1411)  
  
 <400> 4  
 gtcgacccac gcgtccggtg gaagtataat actttgtcat tatgag atg tcg tct 55  
 Met Ser Ser  
 1  
 ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg cag ttt ttt 103  
 Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu Gln Phe Phe  
 5 10 15  
 gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga gcc aaa tgg 151  
 Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg Ala Lys Trp  
 20 25 30 35  
 ata tca cag gac aag gag gtg gct gta aag aag ctc ctc aaa ata gag 199  
 Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu Lys Ile Glu  
 40 45 50  
 aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac atc atc cag 247  
 Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn Ile Ile Gln  
 55 60 65  
 ttt tat gga gta att ctt gaa cct ccc aac tat ggc att gtc aca gaa 295  
 Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile Val Thr Glu  
 70 75 80



87

tat gct tct ctg gga tca ctc tat gat tac att aac agt aac aga agt	343
Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser Asn Arg Ser	
85 90 95	
gag gag atg gat atg gat cac att atg acc tgg gcc act gat gta gcc	391
Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr Asp Val Ala	
100 105 110 115	
aaa gga atg cat tat tta cat atg gag gct cct gtc aag gtg att cac	439
Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys Val Ile His	
120 125 130	
aga gac ctc aag tca aga aac gtt gtt ata gct gct gat gga gta ctg	487
Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp Gly Val Leu	
135 140 145	
aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat aca aca cac	535
Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His Thr Thr His	
150 155 160	
atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa gtt atc cag	583
Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu Val Ile Gln	
165 170 175	
agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat ggt gtg gtt	631
Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr Gly Val Val	
180 185 190 195	
ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt ttg gaa gga	679
Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly Leu Glu Gly	
200 205 210	
tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga tta acc att	727
Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg Leu Thr Ile	
215 220 225	
cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat cag tgt tgg	775
Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His Gln Cys Trp	
230 235 240	
gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc att tca atc	823
Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile Ile Ser Ile	
245 250 255	
ctg gag tcc atg tca aat gac acg agc ctt cct gac aag tgt aac tca	871
Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys Cys Asn Ser	
260 265 270 275	
ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag gca act ctt	919
Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu Ala Thr Leu	
280 285 290	
gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag gag cag gag	967
Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys Glu Gln Glu	
295 300 305	

88

ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa aag ctg aca 1015  
 Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln Lys Leu Thr  
 310 315 320

gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca aga atg tct 1063  
 Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala Arg Met Ser  
 325 330 335

gag gag tct tac ttt gaa tct aaa aca gag gag tca aac agt gca gag 1111  
 Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn Ser Ala Glu  
 340 345 350 355

atg tca tgt cag atc aca gca aca agt aac ggg gag ggc cat ggc atg 1159  
 Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly His Gly Met  
 360 365 370

aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg gat atc ttc 1207  
 Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly Asp Ile Phe  
 375 380 385

tca atg aac aaa gca gga gct gtg atg cat tct ggg atg cag ata aac 1255  
 Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met Gln Ile Asn  
 390 395 400

atg caa gcc aag cag aat tct tcc aaa acc aca tct aag aga agg ggg 1303  
 Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys Arg Arg Gly  
 405 410 415

aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac ttg tca gaa 1351  
 Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp Leu Ser Glu  
 420 425 430 435

ggt gac gat gat gat gat gat gac ggt gag gag gag gat aat gac atg 1399  
 Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp Asn Asp Met  
 440 445 450

gat aat agt gaa tgaaagcaga aagcaaagta ataaaatcac aaatgtttgg 1451  
 Asp Asn Ser Glu  
 455

aaaacacaaa agtaacttgt ttatctcagt ctgtacaaaa acagtaagga ggcagaaagc 1511

caagcactgc attttttaggc caatcacatt tacatgaccg taatttctta tcaattctac 1571

tttttatTTTT gcttacagaa aaacgggggg agaattaagc caaagaagta tatttatgaa 1631

tcagcaaagtg tgggtgcctga ttatagaaat ttgtgatcct atatacaata taggactttt 1691

aaagttgtga cattctggct ttttctttta atgaatactt tttagtttgt atttgacttt 1751

atttccttta ttcaaatcat ttttaaaaaac ttacattttg aacaaacact ctttaactcct 1811

aattgttctt tgacacgtag taattctgtg acatactttt tttttcttat agcaatacac 1871

tgtaatatca gaaatgggtg gcctgagcaa cctagtaaga cctcgtctct actaataatt 1931

aaaaaactag ctggcatggt agcacacacc tgtagtccca gatacttggg aggccaaggc 1991

89

aggaggattg cttgagacct agcaatcagt cagggtcgca gtgagccatg atggcaccac 2051  
 tgcactctag cctgggcaag agaacaagat cctgtctcaa aaaacaaaaa aaaaaaaaaa 2111  
 gggcggccg 2120

<210> 5  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu  
 1 5 10 15  
 Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg  
 20 25 30  
 Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu  
 35 40 45  
 Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn  
 50 55 60  
 Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile  
 65 70 75 80  
 Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser  
 85 90 95  
 Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr  
 100 105 110  
 Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys  
 115 120 125  
 Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp  
 130 135 140  
 Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His  
 145 150 155 160  
 Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu  
 165 170 175  
 Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr  
 180 185 190  
 Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly  
 195 200 205  
 Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg  
 210 215 220  
 Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His

90

225                      230                      235                      240  
 Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile  
                                  245                      250                      255  
 Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys  
                                  260                      265                      270  
 Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu  
                                  275                      280                      285  
 Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys  
                                  290                      295                      300  
 Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln  
 305                      310                      315                      320  
 Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala  
                                  325                      330                      335  
 Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn  
                                  340                      345                      350  
 Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly  
                                  355                      360                      365  
 His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly  
                                  370                      375                      380  
 Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met  
 385                      390                      395                      400  
 Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys  
                                  405                      410                      415  
 Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp  
                                  420                      425                      430  
 Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp  
                                  435                      440                      445  
 Asn Asp Met Asp Asn Ser Glu  
                                  450                      455

&lt;210&gt; 6

&lt;211&gt; 1365

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1365)

&lt;400&gt; 6

atg tcg tct ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg 48  
 Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu

91

1	5	10	15	
cag ttt ttt gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga				96
Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg				
	20	25	30	
gcc aaa tgg ata tca cag gac aag gag gtg gct gta aag aag ctc ctc				144
Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu				
	35	40	45	
aaa ata gag aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac				192
Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn				
	50	55	60	
atc atc cag ttt tat gga gta att ctt gaa cct ccc aac tat ggc att				240
Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile				
	65	70	75	80
gtc aca gaa tat gct tct ctg gga tca ctc tat gat tac att aac agt				288
Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser				
	85	90	95	
aac aga agt gag gag atg gat atg gat cac att atg acc tgg gcc act				336
Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr				
	100	105	110	
gat gta gcc aaa gga atg cat tat tta cat atg gag gct cct gtc aag				384
Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys				
	115	120	125	
gtg att cac aga gac ctc aag tca aga aac gtt gtt ata gct gct gat				432
Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp				
	130	135	140	
gga gta ctg aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat				480
Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His				
	145	150	155	160
aca aca cac atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa				528
Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu				
	165	170	175	
gtt atc cag agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat				576
Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr				
	180	185	190	
ggt gtg gtt ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt				624
Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly				
	195	200	205	
ttg gaa gga tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga				672
Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg				
	210	215	220	
tta acc att cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat				720
Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His				
	225	230	235	240

92

cag tgt tgg gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile 245 250 255	768
att tca atc ctg gag tcc atg tca aat gac acg agc ctt cct gac aag Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys 260 265 270	816
tgt aac tca ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu 275 280 285	864
gca act ctt gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys 290 295 300	912
gag cag gag ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln 305 310 315 320	960
aag ctg aca gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala 325 330 335	1008
aga atg tct gag gag tct tac ttt gaa tct aaa aca gag gag tca aac Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn 340 345 350	1056
agt gca gag atg tca tgt cag atc aca gca aca agt aac ggg gag ggc Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly 355 360 365	1104
cat ggc atg aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly 370 375 380	1152
gat atc ttc tca atg aac aaa gca gga gct gtg atg cat tct ggg atg Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met 385 390 395 400	1200
cag ata aac atg caa gcc aag cag aat tct tcc aaa acc aca tct aag Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys 405 410 415	1248
aga agg ggg aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp 420 425 430	1296
ttg tca gaa ggt gac gat gat gat gat gat gac ggt gag gag gag gat Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp 435 440 445	1344
aat gac atg gat aat agt gaa Asn Asp Met Asp Asn Ser Glu 450 455	1365

93

<210> 7  
 <211> 2454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (51)..(1793)

<400> 7  
 cggtggtggc ggcagcggcg gctgcggggg caccgggccg cggcgccacc atg gcg 56  
 Met Ala  
 1

gtg cga cag gcg ctg ggc cgc ggc ctg cag ctg ggt cga gcg ctg ctg 104  
 Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu  
 5 10 15

ctg cgc ttc acg ggc aag ccc ggc cgg gcc tac ggc ttg ggg cgg ccg 152  
 Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro  
 20 25 30

ggc cgg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg gcc gca 200  
 Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala  
 35 40 45 50

gga cgg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct aac cgt 248  
 Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg  
 55 60 65

ctc cgc ttc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg cgg ttg cag 296  
 Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln  
 70 75 80

cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc ggc cgg 344  
 Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg  
 85 90 95

gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag gaa aaa 392  
 Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys  
 100 105 110

cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc cag gca 440  
 Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala  
 115 120 125 130

att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac acg aga 488  
 Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg  
 135 140 145

cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag tcc att 536  
 Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile  
 150 155 160

ggt aag ggc tgc agt gct gct gtg tat gaa gcc acc atg cct aca ttg 584  
 Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu

94

165	170	175	
ccc cag aac ctg gag gtg Pro Gln Asn Leu Glu Val 180	aca aag agc acc ggg Thr Lys Ser Thr Gly 185	ttg ctt cca ggg aga Leu Leu Pro Gly Arg 190	632
ggc cca ggt acc agt gca Gly Pro Gly Thr Ser 195	cca gga gaa ggg Ala Pro Gly Glu Gly 200	cag gag cga gct ccg ggg Gln Glu Arg Ala Pro Gly 205 210	680
gcc cct gcc ttc ccc ttg Ala Pro Ala Phe Pro 215	gcc atc aag atg atg Ala Ile Lys Met Met 220	tgg aac atc tcg gca Trp Asn Ile Ser Ala 225	728
ggt tcc tcc agc gaa gcc Gly Ser Ser Ser Glu 230	atc ttg aac aca atg Ile Leu Asn Thr Met 235	agc cag gag ctg gtc Ser Gln Glu Leu Val 240	776
cca gcg agc cga gtg gcc Pro Ala Ser Arg Val 245	ttg gct ggg gag tat Leu Ala Gly Glu Tyr 250	gga gca gtc act tac Gly Ala Val Thr Tyr 255	824
aga aaa tcc aag aga ggt Arg Lys Ser Lys Arg 260	ccc aag caa cta gcc Pro Lys Gln Leu Ala 265	cct cac ccc aac atc Pro His Pro Asn Ile 270	872
atc cgg gtt ctc cgc gcc Ile Arg Val Leu Arg 275	ttc acc tct tcc gtg Phe Thr Ser Ser Val 280 285	ccg ctg ctg cca ggg Pro Leu Leu Pro Gly 290	920
gcc ctg gtc gac tac cct Ala Leu Val Asp Tyr 295	gat gtg ctg ccc tca Asp Val Leu Pro Ser 300	cgc ctc cac cct gaa Arg Leu His Pro Glu 305	968
ggc ctg ggc cat ggc cgg Gly Leu Gly His Gly 310	acg ctg ttc ctc gtt Arg Thr Leu Phe Leu 315	atg aag aac tat ccc Val Met Lys Asn Tyr 320	1016
tgt acc ctg cgc cag tac Cys Thr Leu Arg Cln 325	ctt tgt gtg aac aca Leu Cys Val Asn Thr 330	ccc agc ccc cgc ctc Pro Ser Pro Arg Leu 335	1064
gcc gcc atg atg ctg ctg Ala Ala Met Met Leu 340	cag ctg ctg gaa ggc Gln Leu Leu Glu Gly 345 350	gtg gac cat ctg gtt Val Asp His Leu Val 350	1112
caa cag ggc atc gcg cac Gln Gln Gly Ile Ala 355	aga gac ctg aaa tcc His Arg Asp Leu Lys 360 365	gac aac atc ctt gtg Asp Asn Ile Leu Val 370	1160
gag ctg gac cca gac ggc Glu Leu Asp Pro Asp 375	tgc ccc tgg ctg gtg Cys Pro Trp Leu Val 380	atc gca gat ttt ggc Ile Ala Asp Phe Gly 385	1208
tgc tgc ctg gct gat gag Cys Cys Leu Ala Asp 390	agc atc ggc ctg cag Ser Ile Gly Leu Gln 395	ttg ccc ttc agc agc Leu Pro Phe Ser Ser 400	1256



95

tgg tac gtg gat cgg ggc gga aac ggc tgt ctg atg gcc cca gag gtg	1304
Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val	
405 410 415	
tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc aag gct	1352
Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala	
420 425 430	
gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg ctt gtc	1400
Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val	
435 440 445 450	
aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc agc tac	1448
Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr	
455 460 465	
caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca gac gtg	1496
Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val	
470 475 480	
aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag aga cca	1544
Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro	
485 490 495	
tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg ggt gaa	1592
Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu	
500 505 510	
cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt ggc tgg	1640
His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp	
515 520 525 530	
ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc aca gag	1688
Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu	
535 540 545	
aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct aac ctg	1736
Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu	
550 555 560	
gag tgt gaa acg ctc tgc cag gca gcc ctc ctc ctc tgc tca tgg agg	1784
Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg	
565 570 575	
gca gcc ctg tgatgtccct gcatggagct ggtgaattac taaaagaact	1833
Ala Ala Leu	
530	
tggcatactc tgtgtcgtga tggctctgtga atggtgaggg tgggagtcag gagacaagac	1893
agcgcagaga gggctggta gccggaaaag gcctcgggct tggcaaatgg aagaacttga	1953
gtgagagttc agtctgcagt cctctgctca cagacatctg aaaagtgaat ggccaagctg	2013
gtctagtaga tgaggctgga ctgaggaggg gtaggcctgc atccacagag aggatccagg	2073

96

ccaaggcact ggctgtcagt ggcagagttt ggctgtgacc ttgccccta acacgaggaa 2133  
 ctctgttgaa gggggcagcg tagcatgtct gatttgccac ctggatgaag gcagacatca 2193  
 acatgggtca gcacgttcag ttacgggagt gggaaattac atgaggcctg ggcctctgcg 2253  
 ttcccaagct gtgcgttctg gaccagctac tgaattatta atctcactta gcgaaagtga 2313  
 cggatgagca gtaagtaagt aagtgtgggg atttaaactt gagggtttcc ctctgacta 2373  
 gcctctctta caggaattgt gaaatattaa atgcaaattt acaactgcaa aaaaaaaaaa 2433  
 aaaaaaaaaa aagggcggcc c 2454

&lt;210&gt; 8

&lt;211&gt; 581

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala  
 1 5 10 15  
 Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly  
 20 25 30  
 Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp  
 35 40 45  
 Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro  
 50 55 60  
 Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg  
 65 70 75 80  
 Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys  
 85 90 95  
 Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu  
 100 105 110  
 Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile  
 115 120 125  
 Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp  
 130 135 140  
 Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln  
 145 150 155 160  
 Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro  
 165 170 175  
 Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro  
 180 185 190

97

Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala  
 195 200 205  
 Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile  
 210 215 220  
 Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu  
 225 230 235 240  
 Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val  
 245 250 255  
 Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro  
 260 265 270  
 Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu  
 275 280 285  
 Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His  
 290 295 300  
 Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn  
 305 310 315 320  
 Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro  
 325 330 335  
 Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His  
 340 345 350  
 Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile  
 355 360 365  
 Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp  
 370 375 380  
 Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe  
 385 390 395 400  
 Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro  
 405 410 415  
 Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser  
 420 425 430  
 Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly  
 435 440 445  
 Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg  
 450 455 460  
 Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro  
 465 470 475 480  
 Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys  
 485 490 495

98

Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp  
500 505 510

Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val  
515 520 525

Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu  
530 535 540

Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala  
545 550 555 560

Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser  
565 570 575

Trp Arg Ala Ala Leu  
580

&lt;210&gt; 9

&lt;211&gt; 1743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1743)

&lt;400&gt; 9

atg gcg gtg cga cag gcg ctg ggc cgc ggc ctg cag ctg ggt cga gcg 48  
Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala  
1 5 10 15

ctg ctg ctg cgc ttc acg ggc aag ccc ggc cgg gcc tac ggc ttg ggg 96  
Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly  
20 25 30

cgg ccg ggc ccg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg 144  
Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp  
35 40 45

gcc gca gga ccg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct 192  
Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro  
50 55 60

aac cgt ctc cgc ttc ttc cgc cag tdc gtg gcc ggg ctg gcg gcg cgg 240  
Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg  
65 70 75 80

ttg cag cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc 288  
Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys  
85 90 95

ggc cgg gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag 336  
Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu  
100 105 110

99

gaa aaa cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc	384
Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile	
115 120 125	
cag gca att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac	432
Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp	
130 135 140	
acg aga cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag	480
Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln	
145 150 155 160	
tcc att ggt aag ggc tgc agt gct gct gtg tat gaa gcc acc atg cct	528
Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro	
165 170 175	
aca ttg ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca	576
Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro	
180 185 190	
ggg aga ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct	624
Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala	
195 200 205	
ccg ggg gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc	672
Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile	
210 215 220	
tcg gca ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag	720
Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu	
225 230 235 240	
ctg gtc cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc	768
Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val	
245 250 255	
act tac aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc	816
Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro	
260 265 270	
aac atc atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg	864
Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu	
275 280 285	
cca ggg gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac	912
Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His	
290 295 300	
cct gaa ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac	960
Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn	
305 310 315 320	
tat ccc tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc	1008
Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro	
325 330 335	
cgc ctc gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat	1056

100

Arg	Leu	Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His		
			340					345					350				
ctg	gtt	caa	cag	ggc	atc	gcg	cac	aga	gac	ctg	aaa	tcc	gac	aac	atc	1104	
Leu	Val	Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile		
			355				360					365					
ctt	gtg	gag	ctg	gac	cca	gac	ggc	tgc	ccc	tgg	ctg	gtg	atc	gca	gat	1152	
Leu	Val	Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp		
			370				375					380					
ttt	ggc	tgc	tgc	ctg	gct	gat	gag	agc	atc	ggc	ctg	cag	ttg	ccc	ttc	1200	
Phe	Gly	Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe		
						390				395					400		
agc	agc	tgg	tac	gtg	gat	cgg	ggc	gga	aac	ggc	tgt	ctg	atg	gcc	cca	1248	
Ser	Ser	Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro		
				405					410					415			
gag	gtg	tcc	acg	gcc	cgt	cct	ggc	ccc	agg	gca	gtg	att	gac	tac	agc	1296	
Glu	Val	Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser		
				420				425					430				
aag	gct	gat	gcc	tgg	gca	gtg	gga	gcc	atc	gcc	tat	gaa	atc	ttc	ggg	1344	
Lys	Ala	Asp	Ala	Trp	Ala	Val	Gly	Ala	Ile	Ala	Tyr	Glu	Ile	Phe	Gly		
			435				440					445					
ctt	gtc	aat	ccc	ttc	tac	ggc	cag	ggc	aag	gcc	cac	ctt	gaa	agc	cgc	1392	
Leu	Val	Asn	Pro	Phe	Tyr	Gly	Gln	Gly	Lys	Ala	His	Leu	Glu	Ser	Arg		
			450				455				460						
agc	tac	caa	gag	gct	cag	cta	cct	gca	ctg	ccc	gag	tca	gtg	cct	cca	1440	
Ser	Tyr	Gln	Glu	Ala	Gln	Leu	Pro	Ala	Leu	Pro	Glu	Ser	Val	Pro	Pro		
					470					475					480		
gac	gtg	aga	cag	ttg	gtg	agg	gca	ctg	ctc	cag	cga	gag	gcc	agc	aag	1488	
Asp	Val	Arg	Gln	Leu	Val	Arg	Ala	Leu	Leu	Gln	Arg	Glu	Ala	Ser	Lys		
				485				490						495			
aga	cca	tct	gcc	cga	gta	gcc	gca	aat	gtg	ctt	cat	cta	agc	ctc	tgg	1536	
Arg	Pro	Ser	Ala	Arg	Val	Ala	Ala	Asn	Val	Leu	His	Leu	Ser	Leu	Trp		
			500					505					510				
ggt	gaa	cat	att	cta	gcc	ctg	aag	aat	ctg	aag	tta	gac	aag	atg	gtt	1584	
Gly	Glu	His	Ile	Leu	Ala	Leu	Lys	Asn	Leu	Lys	Leu	Asp	Lys	Met	Val		
			515				520					525					
ggc	tgg	ctc	ctc	caa	caa	tcg	gcc	gcc	act	ttg	ttg	gcc	aac	agg	ctc	1632	
Gly	Trp	Leu	Leu	Gln	Gln	Ser	Ala	Ala	Thr	Leu	Leu	Ala	Asn	Arg	Leu		
			530				535					540					
aca	gag	aag	tgt	tgt	gtg	gaa	aca	aaa	atg	aag	atg	ctc	ttt	ctg	gct	1680	
Thr	Glu	Lys	Cys	Cys	Val	Glu	Thr	Lys	Met	Lys	Met	Leu	Phe	Leu	Ala		
					550				555					560			
aac	ctg	gag	tgt	gaa	acg	ctc	tgc	cag	gca	gcc	ctc	ctc	ctc	tgc	tca	1728	
Asn	Leu	Glu	Cys	Glu	Thr	Leu	Cys	Gln	Ala	Ala	Leu	Leu	Leu	Cys	Ser		

101

565 570 575 1743

tgg agg gca gcc ctg  
Trp Arg Ala Ala Leu  
580

<210> 10  
<211> 1864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (275)..(754)

<400> 10  
gtcgaccac gcggtcgccc caccggttcc ggagacatgt ctctgtgttt ctctccctc 60  
cgcttttgag tccgttgaag acacaatttc tctctgtcgg gtgcttagga ggagctccat 120  
gaacatgtat tgaattggac ttagctgaac aggctgctgg ttggctgccc agaggggggca 180  
ggctgtgttg ctgggagcct tccagctccc tgcagcagtc atggggcagg gttccccgag 240  
tccgtaatcc ccatttccac ctactttccc ttag tta ttt gat tcc ctg tct gtc 295  
Leu Phe Asp Ser Leu Ser Val  
1 5

gta ctc agc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag 343  
Val Leu Ser Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln  
10 15 20

gaa aca ctg gca aat atc aca gca gtg agt tac gac ttt gat gag gaa 391  
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu  
25 30 35

ttc ttc agc cag acg agc gag ctg gcc aag gac ttt att cgg aag ctt 439  
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu  
40 45 50 55

ctg gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga 487  
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg  
60 65 70

cac ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cgc agg 535  
His Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg  
75 80 85

gag tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg 583  
Glu Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg  
90 95 100

cgg tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc 631  
Arg Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr  
105 110 115

102

```

cgc tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg 679
Arg Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg
120                      125                      130                      135

aac tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc 727
Asn Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu
                      140                      145                      150

cac cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt 774
His Pro Arg Arg Arg Ser Ser Thr Ser
                      155                      160

ggccgccagg gaggtctggg ccagcgggg ctccttcttg tgcagacttt tggaccacgc 834
tcagcaccag caccggggcg tctgagcac tttgcaagag agatggggcc aaggaattca 894
gaagagcttg caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg 954
ctccagcatt cccaaagctc ttaattctcc ataaaatggg ctttctcttg tctgccatcc 1014
tcagagtctg ggggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc 1074
acggggtgaa ggtcagacta aggcagcctt cttcacaggc tgaggggggtt cagaaccagc 1134
ctggccaaaa attacaccag agagacagag tcttcccat tgggaacagg gtgattgagg 1194
aaagtgaacc ttgggtgtga gggaccaatc ctgtgacctc ccagaaccat ggaagccagg 1254
acgtcaggct gaccaacacc tcagaccttc tgaagcagcc cattgctggc ccgccatgtt 1314
gtaattttgc tcatttttat taaacttctg gtttacctga tgcttggtt cttttagggc 1374
taccctcatc tcatttcctt tagccctgtg gcctgtaact ctgagggggg gcaccagtg 1434
gggtgctgag tgggcagaat ctcagaaggt cctcctgaac cgtccgcgca ggcctgcagt 1494
gggcctgcct cctccttgct tcctaacag gaaggtgtcc agttcaagag aaccaccca 1554
gagactggga gtgggtggctc acgcctataa tccctgcgct ttggcagtcc gaggcagggg 1614
aattgcttga actcaggagt tggagaccag cctgggcaac atggcaaac gcagtctgta 1674
caaaaaatc aaaaaattag ccaggtgtag gggtaggcac ctggcatccc agctactcca 1734
ggggctgagg tgacagcatt gcttaagccc agaaggtcga ggctgcagtg agctgagatc 1794
acgccactgc actccagtct gggtgacaga gagagaccat atccaaaaaa aaaaaaaaaa 1854
gggcggccgc 1864

```

&lt;210&gt; 11

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 11



103

Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro  
1 5 10 15

Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val  
20 25 30

Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala  
35 40 45

Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu  
50 55 60

Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn  
65 70 75 80

Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe  
85 90 95

Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val  
100 105 110

Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu  
115 120 125

Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp  
130 135 140

Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser  
145 150 155 160

<210> 12

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(480)

<400> 12

tta ttt gat tcc ctg tct gtc gta ctc agc tta agt gga gca tcc cct 48  
Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro  
1 5 10 15

ttc ctg gga gac acg aag cag gaa aca ctg gca aat atc aca gca gtc 96  
Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val  
20 25 30

agt tac gac ttt gat gag gaa ttc ttc agc cag acg agc gag ctg gcc 144  
Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala  
35 40 45

aag gac ttt att cgg aag ctt ctg gtt aaa gag acc cgg aaa cgg ctc 192  
Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu  
50 55 60

104

aca atc caa gag gct ctc aga cac ccc tgg atc acg ccg gtg gac aac 240  
 Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn  
 65 70 75 80

cag caa gcc atg gtg cgc agg gag tct gtg gtc aat ctg gag aac ttc 288  
 Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe  
 85 90 95

agg aag cag tat gtc cgc agg cgg tgg aag ctt tcc ttc agc atc gtg 336  
 Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val  
 100 105 110

tcc ctg tgc aac cac ctc acc cgc tcg ctg atg aag aag gtg cac ctg 384  
 Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu  
 115 120 125

agg ccg gat gag gac ctg agg aac tgt gag agt gac act gag gag gac 432  
 Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp  
 130 135 140

atc gcc agg agg aaa gcc ctc cac cca cgg agg agg agc agc acc tcc 480  
 Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser  
 145 150 155 160

&lt;210&gt; 13

&lt;211&gt; 1333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)..(1333)

&lt;400&gt; 13

g acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac 49  
 Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn  
 1 5 10 15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 97  
 Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser  
 20 25 30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat 145  
 Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp  
 35 40 45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct 193  
 Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala  
 50 55 60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg 241  
 Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly  
 65 70 75 80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa 289  
 Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu

105

85										90					95					
gga	acc	ttg	atg	att	aga	gag	acg	tct	gga	gag	aag	aag	cga	tct	ggc	337				
Gly	Thr	Leu	Met	Ile	Arg	Glu	Thr	Ser	Gly	Glu	Lys	Lys	Arg	Ser	Gly					
100					105					110										
cac	agt	gac	agc	aat	ggc	ttt	gct	ggc	cac	atc	aac	ctc	cct	gac	ctg	385				
His	Ser	Asp	Ser	Asn	Gly	Phe	Ala	Gly	His	Ile	Asn	Leu	Pro	Asp	Leu					
115					120					125										
gtg	cag	cag	agc	cat	tct	cca	gct	gga	acc	ccg	act	gag	gga	ctg	ggg	433				
Val	Gln	Gln	Ser	His	Ser	Pro	Ala	Gly	Thr	Pro	Thr	Glu	Gly	Leu	Gly					
130					135					140										
cgc	gtc	tca	acc	cat	tcc	cag	gag	atg	gac	tct	ggg	act	gaa	tat	ggc	481				
Arg	Val	Ser	Thr	His	Ser	Gln	Glu	Met	Asp	Ser	Gly	Thr	Glu	Tyr	Gly					
145	150					155					160									
atg	ggg	agc	agc	acc	aaa	gcc	tcc	ttc	acc	ccc	ttt	gtg	gac	ccc	aga	529				
Met	Gly	Ser	Ser	Thr	Lys	Ala	Ser	Phe	Thr	Pro	Phe	Val	Asp	Pro	Arg					
165					170					175										
gta	tac	cag	acg	tct	ccc	act	gat	gaa	gat	gaa	gag	gat	gag	gaa	tca	577				
Val	Tyr	Gln	Thr	Ser	Pro	Thr	Asp	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Ser					
180					185					190										
tca	gcc	gca	gct	ctg	ttt	act	agc	gaa	ctt	ctt	agg	caa	gaa	cag	gcc	625				
Ser	Ala	Ala	Ala	Leu	Phe	Thr	Ser	Glu	Leu	Leu	Arg	Gln	Glu	Gln	Ala					
195					200					205										
aaa	ctc	aat	gaa	gca	aga	aag	att	tcg	gtg	gta	aat	gta	aac	cca	acc	673				
Lys	Leu	Asn	Glu	Ala	Arg	Lys	Ile	Ser	Val	Val	Asn	Val	Asn	Pro	Thr					
210					215					220										
aac	att	cgg	cct	cat	agc	gac	aca	cca	gaa	atc	aga	aaa	tac	aag	aaa	721				
Asn	Ile	Arg	Pro	His	Ser	Asp	Thr	Pro	Glu	Ile	Arg	Lys	Tyr	Lys	Lys					
225	230					235					240									
cga	ttc	aac	tca	gaa	ata	ctt	tgt	gca	gct	ctg	tgg	ggt	gta	aac	ctt	769				
Arg	Phe	Asn	Ser	Glu	Ile	Leu	Cys	Ala	Ala	Leu	Trp	Gly	Val	Asn	Leu					
245					250					255										
ctg	gtg	ggg	act	gaa	aat	ggc	ctg	atg	ctt	ttg	gac	cga	agt	ggg	caa	817				
Leu	Val	Gly	Thr	Glu	Asn	Gly	Leu	Met	Leu	Leu	Asp	Arg	Ser	Gly	Gln					
260					265					270										
ggc	aaa	gtc	tat	aat	ctg	atc	aac	cgg	agg	cga	ttt	cag	cag	atg	gat	865				
Gly	Lys	Val	Tyr	Asn	Leu	Ile	Asn	Arg	Arg	Arg	Phe	Gln	Gln	Met	Asp					
275					280					285										
gtg	cta	gag	gga	ctg	aat	gtc	ctt	gtg	aca	att	tca	gga	aag	aag	aat	913				
Val	Leu	Glu	Gly	Leu	Asn	Val	Leu	Val	Thr	Ile	Ser	Gly	Lys	Lys	Asn					
290					295					300										
aag	cta	cga	gtt	tac	tat	ctt	tca	tgg	tta	aga	aac	aga	ata	cta	cat	961				
Lys	Leu	Arg	Val	Tyr	Tyr	Leu	Ser	Trp	Leu	Arg	Asn	Arg	Ile	Leu	His					
305	310					315					320									

106

aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac 1009  
 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp  
                   325                  330                  335

ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa 1057  
 Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys  
                   340                  345                  350

ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct 1105  
 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala  
                   355                  360                  365

cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc 1153  
 Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu  
                   370                  375                  380

cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga 1201  
 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg  
                   385                  390                  395                  400

tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt 1249  
 Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val  
                   405                  410                  415

gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc 1297  
 Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly  
                   420                  425                  430

aat atc act cct cat gct att gtc atc ttg cct aaa 1333  
 Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys  
                   435                  440

&lt;210&gt; 14

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn  
   1                  5                  10                  15

Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser  
                   20                  25                  30

Glu Ser Ser Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp  
                   35                  40                  45

Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala  
                   50                  55                  60

Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly  
                   65                  70                  75                  80

Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu  
                   85                  90                  95

107

Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly  
 100 105 110  
 His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu  
 115 120 125  
 Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly  
 130 135 140  
 Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly  
 145 150 155 160  
 Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg  
 165 170 175  
 Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser  
 180 185 190  
 Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala  
 195 200 205  
 Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr  
 210 215 220  
 Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys  
 225 230 235 240  
 Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu  
 245 250 255  
 Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln  
 260 265 270  
 Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp  
 275 280 285  
 Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn  
 290 295 300  
 Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His  
 305 310 315 320  
 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp  
 325 330 335  
 Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys  
 340 345 350  
 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala  
 355 360 365  
 Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu  
 370 375 380  
 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg  
 385 390 395 400

108

Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val  
405 410 415

Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly  
420 425 430

Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys  
435 440

&lt;210&gt; 15

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1332)

&lt;400&gt; 15

acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac 48  
Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn  
1 5 10 15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 96  
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser  
20 25 30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat 144  
Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp  
35 40 45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct 192  
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala  
50 55 60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg 240  
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly  
65 70 75 80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa 288  
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu  
85 90 95

gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc 336  
Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly  
100 105 110

cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg 384  
His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu  
115 120 125

gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg 432  
Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly  
130 135 140

109

cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc	480
Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly	
145 150 155 160	
atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga	528
Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg	
165 170 175	
gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca	576
Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser	
180 185 190	
tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc	624
Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala	
195 200 205	
aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc	672
Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr	
210 215 220	
aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa	720
Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys	
225 230 235 240	
cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt	768
Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu	
245 250 255	
ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa	816
Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln	
260 265 270	
ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat	864
Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp	
275 280 285	
gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat	912
Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn	
290 295 300	
aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat	960
Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His	
305 310 315 320	
aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac	1008
Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp	
325 330 335	
ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa	1056
Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys	
340 345 350	
ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct	1104
Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala	
355 360 365	
cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc	1152

110

Pro	Lys	Pro	Tyr	His	Lys	Phe	Met	Ala	Phe	Lys	Ser	Phe	Ala	Asp	Leu	
370						375					380					
cag	cac	aag	cct	ctg	cta	gtt	gat	ctc	acg	gta	gaa	gaa	ggc	caa	aga	1200
Gln	His	Lys	Pro	Leu	Leu	Val	Asp	Leu	Thr	Val	Glu	Glu	Gly	Gln	Arg	
385						390					395				400	
tta	aag	gtt	att	ttt	ggc	tca	cac	act	ggc	ttc	cat	gta	att	gat	gtt	1248
Leu	Lys	Val	Ile	Phe	Gly	Ser	His	Thr	Gly	Phe	His	Val	Ile	Asp	Val	
				405					410					415		
gat	tca	gga	aac	tct	tat	gat	atc	tac	ata	cca	tct	cat	att	cag	ggc	1296
Asp	Ser	Gly	Asn	Ser	Tyr	Asp	Ile	Tyr	Ile	Pro	Ser	His	Ile	Gln	Gly	
			420					425						430		
aat	atc	act	cct	cat	gct	att	gtc	atc	ttg	cct	aaa					1332
Asn	Ile	Thr	Pro	His	Ala	Ile	Val	Ile	Leu	Pro	Lys					
			435					440								